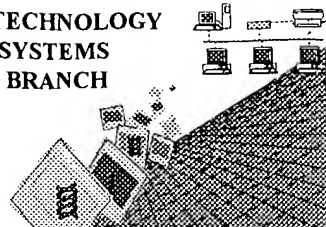


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,313B  
Source: Pg/99  
Date Processed by STIC: 6/12/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/701,313B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,313B

DATE: 06/12/2002

TIME: 14:34:59

Input Set : A:\Lea32701.app

Output Set: N:\CRF3\06122002\I701313B.raw

Does Not Comply  
Corrected Diskette Needed

Corrected Diskette Needed

pp 1-2

cf

5 <110> APPLICANT: Elmar Reinhold Burchardt  
 6 Werner Kroll  
 7 Mathias Gehrman  
 8 Werner Schroder  
 12 <120> TITLE OF INVENTION: Monoclonal antibody and assay for detecting PIIINP  
 16 <130> FILE REFERENCE: MoAb and assay for detecting PIIINP  
 20 <140> CURRENT APPLICATION NUMBER: US/09/701,313B  
 22 <141> CURRENT FILING DATE: 2002-05-11

26 <160> NUMBER OF SEQ ID NOS: 13  
 30 <170> SOFTWARE: PatentIn Ver. 2.0

34 &lt;210&gt; SEQ ID NO: 1

36 &lt;211&gt; LENGTH: 519

38 &lt;212&gt; TYPE: DNA

40 <213> ORGANISM: Primer

44 &lt;400&gt; SEQUENCE: 1

invalid response - see item 10 on Euro Summary sheet

46 atgatgagct ttgtgcaaaa ggggagctgg ctacttctcg ctctgcttca tccactatt 60  
 48 attttggcac aacaggaagc tgttgaagga ggatgttccc atcttggtca gtcctatgcg 120  
 50 gatagagatg tctggaagcc agaaccatgc caaatatgtg tctgtgactc aggatccgtt 180  
 52 ctctgcgatg acataatatg tgacgatcaa gaattagact gcccacccc agaaattcca 240  
 54 tttggagaat gttgtgcagt ttgccacag cctccaactg ctctactcg cctcctaata 300  
 56 ggtcaaggac ctcaaggccc caaggagat ccaggccctc ctggtattcc tgggagaaat 360  
 58 ggtgacctg gtattccagg acaaccaggg tccctgggtt ctctggccc cctggaatc 420  
 60 tgtgaatcat gccctactgg tctcagaac tattctcccc agtatgatc atatgatgc 480  
 62 aagtctggag tagcagtagg aggactcgca ggctatcct 519

66 &lt;210&gt; SEQ ID NO: 2

68 &lt;211&gt; LENGTH: 173

70 &lt;212&gt; TYPE: PRT

72 &lt;213&gt; ORGANISM: Human

76 &lt;400&gt; SEQUENCE: 2

78 Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu  
 80 1 5 10 15  
 84 His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly Gly Cys  
 86 20 25 30  
 90 Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu  
 92 35 40 45  
 96 Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp  
 98 50 55 60  
 102 Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro  
 104 65 70 75 80  
 108 Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr  
 110 85 90 95  
 114 Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly  
 116 100 105 110

## RAW SEQUENCE LISTING

DATE: 06/12/2002

PATENT APPLICATION: US/09/701,313B

TIME: 14:34:59

Input Set : A:\Lea32701.app

Output Set: N:\CRF3\06122002\I701313B.raw

120 Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln  
 122 115 120 125  
 126 Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys  
 128 130 135 140  
 132 Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val  
 134 145 150 155 160  
 138 Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro  
 140 165 170

146 &lt;210&gt; SEQ ID NO: 3

148 &lt;211&gt; LENGTH: 31

150 &lt;212&gt; TYPE: DNA

152 <213> ORGANISM: Primer

156 &lt;220&gt; FEATURE:

158 &lt;223&gt; OTHER INFORMATION: Description of Unknown Organism:Primer

162 &lt;400&gt; SEQUENCE: 3

164 cgcgggtacc aaggggagct ggctacttct c

31

168 &lt;210&gt; SEQ ID NO: 4

170 &lt;211&gt; LENGTH: 30

172 &lt;212&gt; TYPE: DNA

174 <213> ORGANISM: Primer

178 &lt;220&gt; FEATURE:

180 &lt;223&gt; OTHER INFORMATION: Description of Unknown Organism:Primer

184 &lt;400&gt; SEQUENCE: 4

186 cgcgctgcag tgtgactcag gatccgttct

30

190 &lt;210&gt; SEQ ID NO: 5

192 &lt;211&gt; LENGTH: 29

194 &lt;212&gt; TYPE: DNA

196 <213> ORGANISM: Primer

200 &lt;220&gt; FEATURE:

202 &lt;223&gt; OTHER INFORMATION: Description of Unknown Organism:Primer

206 &lt;400&gt; SEQUENCE: 5

208 cgcgaagctt aggggaccct ggttgcct

29

212 &lt;210&gt; SEQ ID NO: 6

214 &lt;211&gt; LENGTH: 31

216 &lt;212&gt; TYPE: DNA

218 <213> ORGANISM: Primer

222 &lt;220&gt; FEATURE:

224 &lt;223&gt; OTHER INFORMATION: Description of Unknown Organism:Primer

228 &lt;400&gt; SEQUENCE: 6

230 cgcgggtacc caggaagctg ttgaaggagg a

31

234 &lt;210&gt; SEQ ID NO: 7

236 &lt;211&gt; LENGTH: 31

238 &lt;212&gt; TYPE: DNA

240 <213> ORGANISM: Primer

244 &lt;220&gt; FEATURE:

246 <223> OTHER INFORMATION: Description of Unknown Organism: Artificial

250 &lt;400&gt; SEQUENCE: 7

252 cgcgaagctt aggatagcct gcgagtcctc c

31

256 &lt;210&gt; SEQ ID NO: 8

(see item 11 on  
Euro summary sheet) but is an  
insufficient  
exploration.

## RAW SEQUENCE LISTING

DATE: 06/12/2002

PATENT APPLICATION: US/09/701,313B

TIME: 14:34:59

Input Set : A:\Lea32701.app

Output Set: N:\CRF3\06122002\I701313B.raw

```

258 <211> LENGTH: 24
260 <212> TYPE: PRT
262 <213> ORGANISM: Human
266 <400> SEQUENCE: 8
268 Met Arg Gly Ser His His His His His His Gly Ser Ala Cys Glu Leu
270   1               5               10               15
274 Gly Thr Gln Glu Ala Val Glu Gly
276               20
282 <210> SEQ ID NO: 9
284 <211> LENGTH: 24
286 <212> TYPE: PRT
288 <213> ORGANISM: Human
292 <400> SEQUENCE: 9
294 Met Arg Gly Ser His His His His His His Gly Ser Ala Cys Glu Leu
296   1               5               10               15
300 Gly Thr Gln Glu Ala Val Glu Gly
302               20
308 <210> SEQ ID NO: 10
310 <211> LENGTH: 24
312 <212> TYPE: PRT
314 <213> ORGANISM: Human
318 <400> SEQUENCE: 10
320 Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala Ser
322   1               5               10               15
326 Ser Val Pro Arg Val Asp Leu Gln
328               20
334 <210> SEQ ID NO: 11
336 <211> LENGTH: 21
338 <212> TYPE: PRT
340 <213> ORGANISM: Human
344 <400> SEQUENCE: 11
346 Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro
348   1               5               10               15
352 Gln Asn Tyr Ser Pro
354               20
360 <210> SEQ ID NO: 12
362 <211> LENGTH: 14
364 <212> TYPE: PRT
366 <213> ORGANISM: Human
370 <400> SEQUENCE: 12
372 Ile Cys Glu Ser Cys Pro Thr Gly Gly Gln Asn Tyr Ser Pro
374   1               5               10
380 <210> SEQ ID NO: 13
382 <211> LENGTH: 30
384 <212> TYPE: DNA
386 <213> ORGANISM: 'Axial Seamount' polynoid polychaete
390 <400> SEQUENCE: 13
392 cgcgaagctt gggagaatag ttctgaggac

```

30

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/701,313B

DATE: 06/12/2002

TIME: 14:35:00

Input Set : A:\Lea32701.app

Output Set: N:\CRF3\06122002\I701313B.raw

L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date